



SEQUENCE LISTING

<10> Elkins, Christopher
<120> ISOLATED POLYNUCLEOTIDES ENCODING DSRA, A PROTEIN CONFERRING
SERUM RESISTANCE TO H. DUCREYI, AND METHODS AND COMPOSITIONS
COMPRISING THE SAME
<130> 5470.269
<140> US 10/030,529
<141> 2002-05-06
<150> PCT/US00/18834
<151> 2000-07-07
<150> US 60/143,257
<151> 1999-07-09
<160> 23
<170> PatentIn version 3.2
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<223> DsrA strain 35000

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tta gtt gcc gta gtg gga tta gct tgt tct act att aca aca atg gct 163
Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr Ile Thr Thr Met Ala
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cag cag ccg cca aag ttt gct gga gta tct tct ttg tat agc tat gag 211
Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu
25 30 35
tat gac tat ggt aag ggt aaa tgg act tgg tct aat gaa ggc ggt ttc 259
Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser Asn Glu Gly Gly Phe
40 45 50
gat att aaa gtg cca ggg att aaa atg aag cca aaa gaa tgg att tct 307
Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro Lys Glu Trp Ile Ser
55 60 65
aaa cag gct act tat ctt gaa tta cag cat tat atg cct tat act cct 355
Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr Met Pro Tyr Thr Pro
70 75 80 85

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tat ccg atg tct gat cct gat caa ctt gga ata aat cgg cag cag ctg	451
Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu	
105 110 115	
aaa ttg aat ttg tat agt tat ttt aac gat tta aga cac gat ttt aaa	499
Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu Arg His Asp Phe Lys	
120 125 130	
tta aaa gtt ctt gat gca cgt att tcc aaa aat aaa caa aat att gat	547
Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp	
135 140 145	
act ata agt aaa tat tta cta gaa ctg ggt act tat tta gat gat tct	595
Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr Tyr Leu Asp Asp Ser	
150 155 160 165	
tat cgt atg atg gaa caa aat aca cat aat atc aat aag ttg tct aaa	643
Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile Asn Lys Leu Ser Lys	
170 175 180	
gaa ttg caa act ggt tta gcc aac caa tca gca ttg tct atg tta gtg	691
Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val	
185 190 195	
caa cca aat ggt gta ggc aaa acg agc gtt tct gct gcg gta gga ggt	739
Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly	
200 205 210	
tat aga gat aaa act gca tta gcc att ggt gtc ggc tca cgc att act	787
Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr	
215 220 225	
gat cgc ttt acc gct aaa gcg ggt gta gcg ttc aat acc tac aat ggc	835
Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly	
230 235 240 245	
ggc atg tct tat ggt gct tct gtt ggt tat gaa ttc taa tcattacggt	884
Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu Phe	
250 255	
taatcactaa tcgttttggt tataataaaa aggctaaatg tttctcctca catttagcct	944
ttcttattta tctttgttat agcttttgct gttataaaac cgtttttttag ccacttttat	1004
taattaagct tttaagccta ttcaatcagt tctactttca cttttttcac catattatcc	1064
gccacttcta aaacggtaat attaagttgg tttagcctaa attgggtacc ttctatcgga	1124
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 <213> Haemophilus ducreyi

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 35 40 45
 Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60
 Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80
 Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
 85 90 95
 Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110
 Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125
 Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140
 Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160
 Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175
 Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 180 185 190
 Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 195 200 205
 Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
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 Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
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Phe

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<212> DNA
<213> Haemophilus ducreyi

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<222> (135)..(926)
<223> DsrA strain CIPA75

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ttaatgaggt gatt atg aaa att aaa tgt tta gtt gcc gta gtg gga tta 170
Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu
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gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt gct 218
Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala
15 20 25
gga gta tct tct ttg tat agc tat gag tat gac tat ggt aag ggt aaa 266
Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys
30 35 40
tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg cca ggg att 314
Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile
45 50 55 60
aaa atg aag cca aaa gaa tgg att tct aaa cag gct act tat ctt gaa 362
Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu
65 70 75
tta cag cat tat atg cct tat act cct gtt ctc gtg aca tat gct cat 410
Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His
80 85 90
gac gtt cct cct agc tct ata ctg tta tat ccg atg tct gat cct gat 458
Asp Val Pro Pro Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp
95 100 105
caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg tat agt tat 506
Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr
110 115 120
ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt gat gca cgt 554
Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg
125 130 135 140
att tcc aaa aat aaa caa aat att gat act ata agt aaa tat tta cta 602

Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu	
145 150 155	
gaa ctg ggt act tat tta gat gat tct tat cgt atg atg gaa caa aat	650
Glu Leu Gly Thr Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn	
160 165 170	
aca cat aat atc aat aaa aat aca cat aat atc aat aag ttg tct aaa	698
Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys	
175 180 185	
gaa ttg caa act ggt tta gcc aac caa tca gca ttg tct atg tta gtg	746
Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val	
190 195 200	
caa cca aat ggt gta ggc aaa acg agc gtt tct gct gcg gta gga ggt	794
Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly	
205 210 215 220	
tat aga gat aaa act gca tta gcc att ggt gtc ggc tca cgc att act	842
Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr	
225 230 235	
gat cgc ttt acc gct aaa gcg ggt gta gcg ttc aat acc tac aat ggc	890
Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly	
240 245 250	
ggc atg tct tat ggt gct tct gtt ggt tat gaa ttc taatcattac	936
Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu Phe	
255 260	
gtttaatcac taatcggtttt gggtataata aaaaggctaa atgtttctcc tcacatttag	996
cctttcttat ttatctttgt tatagctttt gctgttataa aaccgttttt tagccacttt	1056
tattaattaa gcttttaagc ctattcaatc agttctactt tcactttttt caccatatta	1116
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Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60
 Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80
 Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His Asp Val Pro Pro
 85 90 95
 Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110
 Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125
 Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140
 Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160
 Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175
 Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr
 180 185 190
 Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly
 195 200 205
 Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys
 210 215 220
 Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr
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 Gly Ala Ser Val Gly Tyr Glu Phe
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 <213> Haemophilus ducreyi

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 Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu
 1 5 10
 gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt gct 218
 Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala
 15 20 25
 gga gta tct tct ttg tat agc tat gag tat gac tat ggt aag ggt aaa 266
 Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys
 30 35 40
 tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg cca ggg att 314
 Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile
 45 50 55 60
 aaa atg aag cca aaa gaa tgg att tct aaa cag gct act tat ctt gaa 362
 Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu
 65 70 75
 tta cag cat tat atg cct tat act cct gtt ctc gtg aca tat gct cat 410
 Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His
 80 85 90
 gac gtt cct cct agc tct ata ctg tta tat ccg atg tct gat cct gat 458
 Asp Val Pro Pro Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp
 95 100 105
 caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg tat agt tat 506
 Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr
 110 115 120
 ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt gat gca cgt 554
 Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg
 125 130 135 140
 att tcc aaa aat aaa caa aat att gat act ata agt aaa tat tta cta 602
 Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu
 145 150 155
 gaa ctg ggt act tat tta gat gat tct tat cgt atg atg gaa caa aat 650
 Glu Leu Gly Thr Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn
 160 165 170
 aca cat aat atc aat aaa aat aca cat aat atc aat aag ttg tct aaa 698
 Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys
 175 180 185
 gaa ttg caa act ggt tta gcc aac caa tca gca ttg tct atg tta gtg 746
 Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val

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caa cca aat ggt gta ggc aaa acg agc gtt tct gct gcg gta gga ggt			794
Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly			
205	210	215	220
tat aga gat aaa act gca tta gcc att ggt gtc ggc tca cgc att act			842
Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr			
	225	230	235
gat cgc ttt acc gct aaa gcg ggt gta gcg ttc aat acc tac aat ggc			890
Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly			
	240	245	250
ggc atg tct tat ggt gct tct gtt ggt tat gaa ttc taatcattac			936
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Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser			
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Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro			
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Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr			
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Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala His Asp Val Pro Pro			
	85	90	95
Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile			
	100	105	110
Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu			
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Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn			

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Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile		
	165	170 175
Asn Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr		
	180	185 190
Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly		
	195	200 205
Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys		
	210	215 220
Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr		
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Gly Ala Ser Val Gly Tyr Glu Phe		
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<220>
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ttacttaatg aggtgatt atg aaa att aaa tgt tta gtt gcc gta gtg gga	171
Met Lys Ile Lys Cys Leu Val Ala Val Val Gly	
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tta gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt	219
Leu Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe	
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Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly	

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gaa tta cag cat tat atg cct tat act cct gtt ctc gtg aca tat gct Glu Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala 80 85 90			411
cct ggc gtt tct cct agc cct ata ctg tta tat ccg atg tct gat cct Pro Gly Val Ser Pro Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro 95 100 105			459
gat caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg tat agt Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser 110 115 120			507
tat ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt gat gca Tyr Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala 125 130 135			555
cgt att tcc aaa aat aaa caa aat att gat act ata agt aaa tat tta Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu 140 145 150 155			603
cta gaa ctg ggt act tat tta gat gat tct tat cgt atg atg gaa caa Leu Glu Leu Gly Thr Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln 160 165 170			651
aat aca cat aat atc aat aag ttg tct aaa gaa ttg caa act ggt tta Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu 175 180 185			699
gcc aac caa tca gca ttg tct atg tta gtg caa cca aat ggt gta ggc Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly 190 195 200			747
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35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
210 215 220

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
225 230 235 240

Asn Thr Phe Tyr Arg Asn Phe Phe
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<212> DNA
<213> Haemophilus ducreyi

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<222> (147)..(917)
<223> DsrA strain CIP542 (CDC)

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acaattattt acttaatgag gtgatt atg aaa att aaa tgt tta gtt gcc gta 173
Met Lys Ile Lys Cys Leu Val Ala Val
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gtg gga tta gct tgt tct act att aca aca atg gct cag cag ccg cca 221
Val Gly Leu Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro
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aag ttt gct gga gta tct tct ttg tat agc tat gag tat gac tat ggt 269
Lys Phe Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly
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aag ggt aaa tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg 317
Lys Gly Lys Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val
45 50 55
cca ggg att aaa atg aag cca aaa gaa tgg att tct aaa cag gct act 365
Pro Gly Ile Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr
60 65 70
tat ctt gaa tta cag cat tat atg cct tat act cct gtt ctc gtg aca 413
Tyr Leu Glu Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr
75 80 85
tat gct cct ggc gtt tct cct agc cct ata ctg tta tat ccg atg tct 461
Tyr Ala Pro Gly Val Ser Pro Ser Pro Ile Leu Leu Tyr Pro Met Ser
90 95 100 105
gat cct gat caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg 509
Asp Pro Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu
110 115 120
tat agt tat ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt 557
Tyr Ser Tyr Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu
125 130 135
gat gca cgt att tcc aaa aat aaa caa aat att gat act ata agt aaa 605
Asp Ala Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys
140 145 150

tat tta cta gaa ctg ggt act tat tta gat gat tct tat cgt atg atg Tyr Leu Leu Glu Leu Gly Thr Tyr Leu Asp Asp Ser Tyr Arg Met Met 155 160 165	653
gaa caa aat aca cat aat atc aat aag ttg tct aaa gaa ttg caa act Glu Gln Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr 170 175 180 185	701
ggg tta gcc aac caa tca gca ttg tct atg tta gtg caa cca aat ggt Gly Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly 190 195 200	749
gta ggc aaa acg agc gtt tct gct gcg gta gga ggt tat aga gat aaa Val Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys 205 210 215	797
act gca tta gcc att ggt gtc ggc tca cgc att act gat cgc ttt acc Thr Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr 220 225 230	845
gct aaa gcg ggt gta gcg ttc aat acc tac aat ggc ggc atg tct tat Ala Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr 235 240 245	893
ggg gct tct gtt ggt tat gaa ttc taatcattac gtttaatcac taatcgtttt Gly Ala Ser Val Gly Tyr Glu Phe 250 255	947
gggtataata aaaaggctaa atgtttctcc tcacatttag cctttcttat ttatctttgt	1007
tatagccttt tgctgttata aaacggtttt ttagccactt ttattaatta agctttttaag	1067
cctattcaat cagttctact ttcacttttt tcaccatatt atccgccact tctaaaacgg	1127
taatattaag ttgggttagc cttaaattggg taccttctat cggaattttt tctaaatggt	1187
ctaaaattaa	1197
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser 20 25 30	
Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser 35 40 45	
Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro 50 55 60	

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
85 90 95

Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
145 150 155 160

Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
165 170 175

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
180 185 190

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
195 200 205

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
210 215 220

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
225 230 235 240

Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
245 250 255

Phe

<210> 11
<211> 923
<212> DNA
<213> Haemophilus ducreyi

<220>

<221> CDS
 <222> (45)..(833)
 <223> DsrA strain CHIA

<400> 11

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Met Lys Ile Lys	
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tgt tta gtt gcc gta gtg gga tta gct tgt tct act att aca aca atg	104
Cys Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr Ile Thr Thr Met	
5 10 15 20	
gct cag cag ccg cca aag ttt gct gga gta tct tct ttg gat agc tat	152
Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser Leu Asp Ser Tyr	
25 30 35	
gag tat gac tat ggt aag ggt aaa tgg act tgg tct gaa aaa gac ggt	200
Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser Glu Lys Asp Gly	
40 45 50	
ttc gat att aaa gcg cca ggg att aaa atg aag cca aaa aaa tgg att	248
Phe Asp Ile Lys Ala Pro Gly Ile Lys Met Lys Pro Lys Lys Trp Ile	
55 60 65	
tct aga cag gct act tat ctt gga tta cag cat tat atg cct tat act	296
Ser Arg Gln Ala Thr Tyr Leu Gly Leu Gln His Tyr Met Pro Tyr Thr	
70 75 80	
cct gtt ctc gtg aca tat gct tct gca gaa cct aac act gta ctg tta	344
Pro Val Leu Val Thr Tyr Ala Ser Ala Glu Pro Asn Thr Val Leu Leu	
85 90 95 100	
tat ccg atg cct gat cct gat caa ctt gga ata aat cgg cag cag ctg	392
Tyr Pro Met Pro Asp Pro Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu	
105 110 115	
aaa ttg aat ttg tat agt tat ttt aac gat tta aga cac ggt ttt aaa	440
Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu Arg His Gly Phe Lys	
120 125 130	
tta aat gtt ctt gat gca cgt att tcc caa aat aaa caa aat att gat	488
Leu Asn Val Leu Asp Ala Arg Ile Ser Gln Asn Lys Gln Asn Ile Asp	
135 140 145	
act ata agt gaa tat tta cta aaa ctg ggt act tat tta gat agt tct	536
Thr Ile Ser Glu Tyr Leu Leu Lys Leu Gly Thr Tyr Leu Asp Ser Ser	
150 155 160	
tat cgt atg atg gaa caa aat aca cat aat atc aat aaa aat aca cat	584
Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile Asn Lys Asn Thr His	
165 170 175 180	
aat atc aat aag ttg tct aaa gaa ttg caa act ggt tta gcc aac caa	632
Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln	
185 190 195	
tca gca ttg tct atg tta gtg caa cca aat ggt gta ggc aaa acg agc	680
Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser	
200 205 210	

gtt tct gct gcg gta gga ggt tat aga gat aaa act gca tta gcc att 728
 Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile
 215 220 225

ggt gtc ggc tca cgc att act gat cgc ttt acc gct aaa gcg ggt gta 776
 Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val
 230 235 240

gcg ttc aat acc tac aat ggc ggc atg tct tat ggt gct tct gtt ggt 824
 Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly
 245 250 255 260

tat gaa ttc taatcattac gtttaatcac taatcgtttt gggtataata 873
 Tyr Glu Phe

aaaaggctaa atgtttctcc tcacatttag cctttcttat ttatctttgt 923

<210> 12
 <211> 263
 <212> PRT
 <213> Haemophilus ducreyi

<400> 12

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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
 20 25 30

Leu Asp Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Glu Lys Asp Gly Phe Asp Ile Lys Ala Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Lys Trp Ile Ser Arg Gln Ala Thr Tyr Leu Gly Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Ser Ala Glu Pro Asn
 85 90 95

Thr Val Leu Leu Tyr Pro Met Pro Asp Pro Asp Gln Leu Gly Ile Asn
 100 105 110

Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu Arg
 115 120 125

His Gly Phe Lys Leu Asn Val Leu Asp Ala Arg Ile Ser Gln Asn Lys
 130 135 140

Gln Asn Ile Asp Thr Ile Ser Glu Tyr Leu Leu Lys Leu Gly Thr Tyr
 145 150 155 160

Leu Asp Ser Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile Asn
 165 170 175

Lys Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly
 180 185 190

Leu Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val
 195 200 205

Gly Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr
 210 215 220

Ala Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala
 225 230 235 240

Lys Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly
 245 250 255

Ala Ser Val Gly Tyr Glu Phe
 260

<210> 13
 <211> 1231
 <212> DNA
 <213> Haemophilus ducreyi

<220>
 <221> CDS
 <222> (140)..(952)
 <223> DsrA strain V-1157

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 ttttaatgta aggtagaata agaaagtaaa ttctatatattt acaatcaaga ttgacaatta 120
 tttacttaat gaggtgatt atg aaa att aaa tgt tta gtt gcc gta gtg gga 172
 Met Lys Ile Lys Cys Leu Val Ala Val Val Gly
 1 5 10
 tta gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt 220
 Leu Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe
 15 20 25
 gct gga gta tct tct ttg tat agc tat gag tat gac tat ggt aag ggt 268
 Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly
 30 35 40

aaa tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg cca ggg Lys Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly 45 50 55	316
att aaa atg aag cca aaa gaa tgg att tct aaa cag gct act tat ctt Ile Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu 60 65 70 75	364
gaa tta cag cat tat atg cct tat act cct gtt ctc gtg aca tct gct Glu Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala 80 85 90	412
cct gac gtt cct cct agc tct ata ctg tta tat ccg atg tct gat cct Pro Asp Val Pro Pro Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro 95 100 105	460
gat caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg tat agt Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser 110 115 120	508
tat ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt gat gca Tyr Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala 125 130 135	556
cgt att tcc aaa aat aaa caa aat att gat act ata agt aaa tat tta Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu 140 145 150 155	604
cta gaa ctg ggt act tat tta gat ggt tct tat cgt atg atg gaa caa Leu Glu Leu Gly Thr Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln 160 165 170	652
aat aca cat aat atc aat aaa aat aca cat aat atc aat aaa aat aca Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr 175 180 185	700
cat aat atc aat aag ttg tct aaa gaa ttg caa act ggt tta gcc aac His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn 190 195 200	748
caa tca gca ttg tct atg tta gtg caa cca aat ggt gta ggc aaa acg Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr 205 210 215	796
agc gtt tct gct gcg gta gga ggt tat aga gat aaa act gca tta gcc Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala 220 225 230 235	844
att ggt gtc ggc tca cgc att act gat cgc ttt acc gct aaa gcg ggt Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly 240 245 250	892
gta gcg ttc aat acc tac aat ggc ggc atg tct tat ggt gct tct gtt Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val 255 260 265	940
ggt tat gaa ttc taatcattac gtttaatcac taatcgtttt gggtataata Gly Tyr Glu Phe 270	992
aaaaggctaa atgttttctcc tcacatttag ccttttcttat ttatctttgt tatagctttt	1052

gctgttataa aaccgttttt tagccacttt tattaattaa gcttttaagc ctattcaatc 1112
 agttctactt tcaactttttt caccatatta tccgccactt ctaaaacggt aatattaagt 1172
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<210> 14
 <211> 271
 <212> PRT
 <213> Haemophilus ducreyi

<400> 14

Met Lys Ile Lys Cys Leu Val Ala Val Val Gly Leu Ala Cys Ser Thr
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
 20 25 30

Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala Pro Asp Val Pro Pro
 85 90 95

Ser Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110

Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125

Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140

Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160

Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175

Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys
 180 185 190

Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala Leu Ser
 195 200 205

Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser Ala Ala
 210 215 220

Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val Gly Ser
 225 230 235 240

Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe Asn Thr
 245 250 255

Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu Phe
 260 265 270

<210> 15
 <211> 1047
 <212> DNA
 <213> Haemophilus ducreyi

<220>
 <221> CDS
 <222> (140)..(958)
 <223> DsrA strain M90-02

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 tttacttaat gaggtgatt atg aaa att aaa tgt tta gtt gcc gta gtg gga 172
 Met Lys Ile Lys Cys Leu Val Ala Val Val Gly
 1 5 10
 tta gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt 220
 Leu Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe
 15 20 25
 gct gga gta tct tct ttg tat agc tat gag tat gac tat ggt aag ggt 268
 Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly
 30 35 40
 aaa tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg cca ggg 316
 Lys Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly
 45 50 55
 att aaa atg aag cca aaa gaa tgg att tct aaa cag gct act tat ctt 364
 Ile Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu
 60 65 70 75
 gaa tta cag cat tat atg cct tat act cct gtt ctc gtg aca tct gct 412
 Glu Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala
 80 85 90

cct gac gtt tct cct agc tct atc tct ata ctg tta tat ccg atg tct Pro Asp Val Ser Pro Ser Ser Ile Ser Ile Leu Leu Tyr Pro Met Ser 95 100 105	460
gat cct gat caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg Asp Pro Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu 110 115 120	508
tat agt tat ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt Tyr Ser Tyr Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu 125 130 135	556
gat gca cgt att tcc aaa aat aaa caa aat att gat act ata agt aaa Asp Ala Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys 140 145 150 155	604
tat tta cta gaa ctg ggt act tat tta gat ggt tct tat cgt atg atg Tyr Leu Leu Glu Leu Gly Thr Tyr Leu Asp Gly Ser Tyr Arg Met Met 160 165 170	652
gaa caa aat aca cat aat atc aat aaa aat aca cat aat atc aat aaa Glu Gln Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys 175 180 185	700
aat aca cat aat atc aat aag ttg tct aaa gaa ttg caa act ggt tta Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu 190 195 200	748
gcc aac caa tca gca ttg tct atg tta gtg caa cca aat ggt gta ggc Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly 205 210 215	796
aaa acg agc gtt tct gct gcg gta gga ggt tat aga gat aaa act gca Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala 220 225 230 235	844
tta gcc att ggt gtc ggc tca cgc att act gat cgc ttt acc gct aaa Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys 240 245 250	892
gcg ggt gta gcg ttc aat acc tac aat ggc ggc atg tct tat ggt gct Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala 255 260 265	940
tct gtt ggt tat gaa ttc taatcattac gtttaatcac taatcgtttt Ser Val Gly Tyr Glu Phe 270	988
ggttataata aaaaggctaa atgtttctcc tcacatttag ccttttctta tttatcttt	1047
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser
 20 25 30

Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser
 35 40 45

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60

Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80

Met Pro Tyr Thr Pro Val Leu Val Thr Ser Ala Pro Asp Val Ser Pro
 85 90 95

Ser Ser Ile Ser Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu
 100 105 110

Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn
 115 120 125

Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser
 130 135 140

Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu
 145 150 155 160

Gly Thr Tyr Leu Asp Gly Ser Tyr Arg Met Met Glu Gln Asn Thr His
 165 170 175

Asn Ile Asn Lys Asn Thr His Asn Ile Asn Lys Asn Thr His Asn Ile
 180 185 190

Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 195 200 205

Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 210 215 220

Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
 225 230 235 240

Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
 245 250 255

Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
 260 265 270

Phe

<210> 17
 <211> 1189
 <212> DNA
 <213> Haemophilus ducreyi

<220>
 <221> CDS
 <222> (139)..(909)
 <223> DsrA strain 406

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 ttacttaatg aggtgatt atg aaa att aaa tgt tta gtt gcc gta gtg gga 171
 Met Lys Ile Lys Cys Leu Val Ala Val Val Gly
 1 5 10
 tta gct tgt tct act att aca aca atg gct cag cag ccg cca aag ttt 219
 Leu Ala Cys Ser Thr Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe
 15 20 25
 gct gga gta tct tct ttg tat agc tat gag tat gac tat ggt aag ggt 267
 Ala Gly Val Ser Ser Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly
 30 35 40
 aaa tgg act tgg tct aat gaa ggc ggt ttc gat att aaa gtg cca ggg 315
 Lys Trp Thr Trp Ser Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly
 45 50 55
 att aaa atg aag cca aaa gaa tgg att tct aaa cag gct act tat ctt 363
 Ile Lys Met Lys Pro Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu
 60 65 70 75
 gaa tta cag cat tat atg cct tat act cct gtt ctc gtg aca tat gct 411
 Glu Leu Gln His Tyr Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala
 80 85 90
 cct ggc gtt tct cct agc cct ata ctg tta tat ccg atg tct gat cct 459
 Pro Gly Val Ser Pro Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro
 95 100 105
 gat caa ctt gga ata aat cgg cag cag ctg aaa ttg aat ttg tat agt 507
 Asp Gln Leu Gly Ile Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser
 110 115 120
 tat ttt aac gat tta aga cac gat ttt aaa tta aaa gtt ctt gat gca 555
 Tyr Phe Asn Asp Leu Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala
 125 130 135

cgt att tcc aaa aat aaa caa aat att gat act ata agt aaa tat tta	603
Arg Ile Ser Lys Asn Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu	
140 145 150 155	
cta gaa ctg ggt act tat tta gat gat tct tat cgt atg atg gaa caa	651
Leu Glu Leu Gly Thr Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln	
160 165 170	
aat aca cat aat atc aat aag ttg tct aaa gaa ttg caa act ggt tta	699
Asn Thr His Asn Ile Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu	
175 180 185	
gcc aac caa tca gca ttg tct atg tta gtg caa cca aat ggt gta ggc	747
Ala Asn Gln Ser Ala Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly	
190 195 200	
aaa acg agc gtt tct gct gcg gta gga ggt tat aga gat aaa act gca	795
Lys Thr Ser Val Ser Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala	
205 210 215	
tta gcc att ggt gtc ggc tca cgc att act gat cgc ttt acc gct aaa	843
Leu Ala Ile Gly Val Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys	
220 225 230 235	
gcg ggt gta gcg ttc aat acc tac aat ggc ggc atg tct tat ggt gct	891
Ala Gly Val Ala Phe Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala	
240 245 250	
tct gtt ggt tat gaa ttc taatcattac gtttaatcac taatcgtttt	939
Ser Val Gly Tyr Glu Phe	
255	
ggttataata aaaaggctaa atgtttctcc tcacatttag cctttcttat ttatctttgt	999
tatagctttt gctgttataa aaccgttttt tagccacttt tattaattaa gcttttaagc	1059
ctattcaatc agttctactt tcactttttt caccatatta tccgccactt ctaaaacggt	1119
aatattaagt tggtttagcc taaattgggt accttctatc ggaatttttt cttaatgttc	1179
taaaattaag	1189
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<211> 257	
<212> PRT	
<213> Haemophilus ducreyi	
<400> 18	
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Ile Thr Thr Met Ala Gln Gln Pro Pro Lys Phe Ala Gly Val Ser Ser	
20 25 30	
Leu Tyr Ser Tyr Glu Tyr Asp Tyr Gly Lys Gly Lys Trp Thr Trp Ser	
35 40 45	

Asn Glu Gly Gly Phe Asp Ile Lys Val Pro Gly Ile Lys Met Lys Pro
 50 55 60
 Lys Glu Trp Ile Ser Lys Gln Ala Thr Tyr Leu Glu Leu Gln His Tyr
 65 70 75 80
 Met Pro Tyr Thr Pro Val Leu Val Thr Tyr Ala Pro Gly Val Ser Pro
 85 90 95
 Ser Pro Ile Leu Leu Tyr Pro Met Ser Asp Pro Asp Gln Leu Gly Ile
 100 105 110
 Asn Arg Gln Gln Leu Lys Leu Asn Leu Tyr Ser Tyr Phe Asn Asp Leu
 115 120 125
 Arg His Asp Phe Lys Leu Lys Val Leu Asp Ala Arg Ile Ser Lys Asn
 130 135 140
 Lys Gln Asn Ile Asp Thr Ile Ser Lys Tyr Leu Leu Glu Leu Gly Thr
 145 150 155 160
 Tyr Leu Asp Asp Ser Tyr Arg Met Met Glu Gln Asn Thr His Asn Ile
 165 170 175
 Asn Lys Leu Ser Lys Glu Leu Gln Thr Gly Leu Ala Asn Gln Ser Ala
 180 185 190
 Leu Ser Met Leu Val Gln Pro Asn Gly Val Gly Lys Thr Ser Val Ser
 195 200 205
 Ala Ala Val Gly Gly Tyr Arg Asp Lys Thr Ala Leu Ala Ile Gly Val
 210 215 220
 Gly Ser Arg Ile Thr Asp Arg Phe Thr Ala Lys Ala Gly Val Ala Phe
 225 230 235 240
 Asn Thr Tyr Asn Gly Gly Met Ser Tyr Gly Ala Ser Val Gly Tyr Glu
 245 250 255

Phe

<210> 19
 <211> 7
 <212> PRT
 <213> Haemophilus ducreyi

<400> 19

Asn Thr His Asn Ile Asn Lys
1 5

<210> 20

<211> 547

<212> PRT

<213> Moraxella catarrhalis

<400> 20

Gln Val Val Glu Gln Phe Phe Pro Asn Ile Phe Phe Asn Glu Asn His
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Asp Glu Leu Asp Asp Ala Tyr His Asn Met Ile Leu Gly Asp Thr Ala
20 25 30

Ile Val Ser Asn Ser Gln Asp Asn Ser Thr Gln Leu Lys Phe Tyr Ser
35 40 45

Asn Asp Glu Asp Ser Val Pro Asp Ser Leu Leu Phe Ser Lys Leu Leu
50 55 60

His Glu Gln Gln Leu Asn Gly Phe Lys Ala Gly Asp Thr Ile Ile Pro
65 70 75 80

Leu Asp Lys Asp Gly Lys Pro Val Tyr Thr Lys Asp Thr Arg Thr Lys
85 90 95

Asp Gly Lys Val Glu Thr Val Tyr Ser Val Thr Thr Lys Ile Ala Thr
100 105 110

Gln Asp Asp Val Glu Gln Ser Ala Tyr Ser Arg Gly Ile Gln Gly Asp
115 120 125

Ile Asp Asp Leu Tyr Asp Ile Asn Arg Glu Val Asn Glu Tyr Leu Lys
130 135 140

Ala Thr His Asp Tyr Asn Glu Arg Gln Thr Glu Ala Ile Asp Ala Leu
145 150 155 160

Asn Lys Ala Ser Ser Ala Asn Thr Asp Arg Ile Asp Thr Ala Glu Glu
165 170 175

Arg Ile Asp Lys Asn Glu Tyr Asp Ile Lys Ala Leu Glu Ser Asn Val
180 185 190

Glu Glu Gly Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala
 195 200 205

Asp Leu Thr Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly
 210 215 220

Leu Leu Glu Leu Ser Gly His Leu Ile Asp Gln Lys Ala Asp Leu Thr
 225 230 235 240

Lys Asp Ile Lys Ala Leu Glu Ser Asn Val Glu Glu Gly Leu Leu Asp
 245 250 255

Leu Ser Gly Arg Leu Leu Asp Gln Lys Ala Asp Ile Ala Lys Asn Gln
 260 265 270

Ala Asp Ile Ala Gln Asn Gln Thr Asp Ile Gln Asp Leu Ala Ala Tyr
 275 280 285

Asn Glu Leu Gln Asp Ala Tyr Ala Lys Gln Gln Thr Glu Ala Ile Asp
 290 295 300

Ala Leu Asn Lys Ala Ser Ser Glu Asn Thr Gln Asn Ile Ala Lys Asn
 305 310 315 320

Gln Ala Asp Ile Ala Asn Asn Ile Asn Asn Ile Tyr Glu Leu Ala Gln
 325 330 335

Gln Gln Asp Gln His Ser Ser Asp Ile Lys Thr Leu Ala Lys Ala Ser
 340 345 350

Ala Ala Asn Thr Asp Arg Ile Ala Lys Asn Lys Ala Asp Ala Asp Ala
 355 360 365

Ser Phe Glu Thr Leu Thr Lys Asn Gln Asn Thr Leu Ile Glu Lys Asp
 370 375 380

Lys Glu His Asp Lys Leu Ile Thr Ala Asn Lys Thr Ala Ile Asp Ala
 385 390 395 400

Asn Lys Ala Ser Ala Asp Thr Lys Phe Ala Ala Thr Ala Asp Ala Ile
 405 410 415

Thr Lys Asn Gly Asn Ala Ile Thr Lys Asn Ala Lys Ser Ile Thr Asp
 420 425 430

Leu Gly Thr Lys Val Asp Gly Phe Asp Gly Arg Val Thr Ala Leu Asp
 435 440 445

Thr Lys Val Asn Ala Leu Asp Thr Lys Val Asn Ala Phe Asp Gly Arg
 450 455 460

Ile Thr Ala Leu Asp Ser Lys Val Glu Asn Gly Met Ala Ala Gln Ala
 465 470 475 480

Ala Leu Ser Gly Leu Phe Gln Pro Tyr Ser Val Gly Lys Phe Asn Ala
 485 490 495

Thr Ala Ala Leu Gly Gly Tyr Gly Ser Lys Ser Ala Val Ala Ile Gly
 500 505 510

Ala Gly Tyr Arg Val Asn Pro Asn Leu Ala Phe Lys Ala Gly Ala Ala
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Ile Asn Thr Ser Gly Asn Lys Lys Gly Ser Tyr Asn Ile Gly Val Asn
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Tyr Glu Phe
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Pro Gly Ala Gly Gly Leu Asn Ala Ser Ala Lys Gly Ile His Ser Ile
 35 40 45

Ala Ile Gly Ala Thr Ala Glu Ala Ala Lys Gly Ala Ala Val Ala Val
 50 55 60

Gly Ala Gly Ser Ile Ala Thr Gly Val Asn Ser Val Ala Ile Gly Pro
 65 70 75 80

Leu Ser Lys Ala Leu Gly Asp Ser Ala Val Thr Tyr Gly Ala Ala Ser
 85 90 95

Thr Ala Gln Lys Asp Gly Val Ala Ile Gly Ala Arg Ala Ser Thr Ser
100 105 110

Asp Thr Gly Val Ala Val Gly Phe Asn Ser Lys Ala Asp Ala Lys Asn
115 120 125

Ser Val Ala Ile Gly His Ser Ser His Val Ala Ala Asn His Gly Tyr
130 135 140

Ser Ile Ala Ile Gly Asp Arg Ser Lys Thr Asp Arg Glu Asn Ser Val
145 150 155 160

Ser Ile Gly His Glu Ser Leu Asn Arg Gln Leu Thr His Leu Ala Ala
165 170 175

Gly Thr Lys Asp Thr Asp Ala Val Asn Val Ala Gln Leu Lys Lys Glu
180 185 190

Ile Glu Lys Thr Gln Glu Asn Thr Asn Lys Arg Ser Ala Glu Leu Leu
195 200 205

Ala Asn Ala Asn Ala Tyr Ala Asp Asn Lys Ser Ser Ser Val Leu Gly
210 215 220

Ile Ala Asn Asn Tyr Thr Asp Ser Lys Ser Ala Glu Thr Leu Glu Asn
225 230 235 240

Ala Arg Lys Glu Ala Phe Ala Gln Ser Lys Asp Val Leu Asn Met Ala
245 250 255

Lys Ala His Ser Asn Ser Val Ala Arg Thr Thr Leu Glu Thr Ala Glu
260 265 270

Glu His Ala Asn Ser Val Ala Arg Thr Thr Leu Glu Thr Ala Glu Glu
275 280 285

His Ala Asn Lys Lys Ser Ala Glu Ala Leu Ala Ser Ala Asn Val Tyr
290 295 300

Ala Asp Ser Lys Ser Ser His Thr Leu Lys Thr Ala Asn Ser Tyr Thr
305 310 315 320

Asp Val Thr Val Ser Asn Ser Thr Lys Lys Ala Ile Arg Glu Ser Asn
325 330 335

Gln Tyr Thr Asp His Lys Phe Arg Gln Leu Asp Asn Arg Leu Asp Lys
 340 345 350

Leu Asp Thr Arg Val Asp Lys Gly Leu Ala Ser Ser Ala Ala Leu Asn
 355 360 365

Ser Leu Phe Gln Pro Tyr Gly Val Gly Lys Val Asn Phe Thr Ala Gly
 370 375 380

Val Gly Gly Tyr Arg Ser Ser Gln Ala Leu Ala Ile Gly Ser Gly Tyr
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Arg Val Asn Glu Asn Val Ala Leu Lys Ala Gly Val Ala Tyr Ala Gly
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